



SEQUENCE LISTING

<110> Kilian, Andrzej
Bowtell, David

<120> VERTEBRATE TELOMERASE GENES AND PROTEINS AND USES
THEREOF

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<140> 09/502,424

<141> 2000-02-11

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 35 40 45
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 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
 85 90 95
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro

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 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
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 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
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 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
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 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
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 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
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 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
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 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
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 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
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 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
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 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
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D10

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 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
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 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
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 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
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 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
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 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
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 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
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 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
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D10

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 Gln Tyr Pro Thr Leu Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu
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D10

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Leu Asn Ser Ile Cys Pro Pro Leu Glu Gly Thr Val Leu Asp Leu Ser
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His Leu Ser Arg Gln Ser Pro Lys Glu Arg Val Leu Lys Phe Ile Ile
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Val Ile Leu Gln Lys Leu Leu Pro Gln Glu Met Phe Gly Ser Lys Lys
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Asn Lys Gly Lys Ile Ile Lys Asn Leu Asn Leu Leu Leu Ser Leu Pro
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Leu Asn Gly Tyr Leu Pro Phe Asp Ser Leu Leu Lys Lys Leu Arg Leu
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Lys Asp Phe Arg Trp Leu Phe Ile Ser Asp Ile Trp Phe Thr Lys His
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Asn Phe Glu Asn Leu Asn Gln Leu Ala Ile Cys Phe Ile Ser Trp Leu
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Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr Phe Lys Thr Tyr Leu

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 Ser Gln Tyr Phe Phe Asn Thr Asn Thr Gly Val Leu Lys Leu Phe Asn
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 Val Val Asn Ala Ser Arg Val Pro Lys Pro Tyr Glu Leu Tyr Ile Asp
 580 585 590
 Asn Val Arg Thr Val His Leu Ser Asn Gln Asp Val Ile Asn Val Val
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 Glu Met Glu Ile Phe Lys Thr Ala Leu Trp Val Glu Asp Lys Cys Tyr
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 Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro Ile
 625 630 635 640
 Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe Lys
 645 650 655
 Ala Ser Pro Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe
 660 665 670
 Leu Ile Ile Ser Thr Asp Gln Gln Gln Val Ile Asn Ile Lys Lys Leu
 675 680 685
 Ala Met Gly Gly Phe Gln Lys Tyr Asn Ala Lys Ala Asn Arg Asp Lys
 690 695 700
 Ile Leu Ala Val Ser Ser Gln Ser Asp Asp Thr Val Ile Gln Phe
 705 710 715 720

D10

Cys Ala Met His Ile Phe Val Lys Glu Leu Glu Val Trp Lys His Ser
 725 730 735
 Ser Thr Met Asn Asn Phe His Ile Arg Ser Lys Ser Ser Lys Gly Ile
 740 745 750
 Phe Arg Ser Leu Ile Ala Leu Phe Asn Thr Arg Ile Ser Tyr Lys Thr
 755 760 765
 Ile Asp Thr Asn Leu Asn Ser Thr Asn Thr Val Leu Met Gln Ile Asp
 770 775 780
 His Val Val Lys Asn Ile Ser Glu Cys Tyr Lys Ser Ala Phe Lys Asp
 785 790 795 800
 Leu Ser Ile Asn Val Thr Gln Asn Met Gln Phe His Ser Phe Leu Gln
 805 810 815
 Arg Ile Ile Glu Met Thr Val Ser Gly Cys Pro Ile Thr Lys Cys Asp
 820 825 830
 Pro Leu Ile Glu Tyr Glu Val Arg Phe Thr Ile Leu Asn Gly Phe Leu
 835 840 845
 Glu Ser Leu Ser Ser Asn Thr Ser Lys Phe Lys Asp Asn Ile Ile Leu
 850 855 860
 Leu Arg Lys Glu Ile Gln His Leu Gln Ala Tyr Ile Tyr Ile Tyr Ile
 865 870 875 880
 His Ile Val Asn

D10

<210> 6
 <211> 13
 <212> DNA
 <213> Homo sapiens

<220>
 <221> intron
 <222> (8)..(13)
 <223> First six bases of Y intron

<400> 6
 ccaggtgggc ctc

13

<210> 7
 <211> 14
 <212> DNA
 <213> Homo sapiens

<220>
 <221> intron
 <222> (1)..(7)
 <223> Last seven bases of intron Y

<400> 7
gcaggtgtcc tgcc

14

<210> 8
<211> 14
<212> DNA
<213> Homo sapiens

<220>
<221> intron
<222> (8)..(14)
<223> First 7 bases of Intron 1

<400> 8
aaagagggtg gctg

14

<210> 9
<211> 14
<212> DNA
<213> Homo sapiens

<220>
<221> intron
<222> (1)..(7)
<223> Last 7 bases of Intron 1

P10
<400> 9
aacagaagcc gagc

14

<210> 10
<211> 14
<212> DNA
<213> Homo sapiens

<220>
<221> intron
<222> (8)..(14)
<223> First 7 bases of Intron Alpha

<400> 10
tgtcaagggtg gatg

14

<210> 11
<211> 14
<212> DNA
<213> Homo sapiens

<220>
<221> intron
<222> (1)..(7)
<223> Last 7 bases of Intron Alpha

<400> 11
ccccaggac aggc

14

<210> 12
<211> 14
<212> DNA

<213> Homo sapiens

<220>

<221> intron

<222> (8)..(14)

<223> First 7 bases of Intron Beta

<400> 12

gagccacgtc tcta

14

<210> 13

<211> 14

<212> DNA

<213> Homo sapiens

<220>

<221> intron

<222> (1)..(7)

<223> Last 7 bases of Intron Beta

<400> 13

ggggcaagtc ctac

14

<210> 14

<211> 14

<212> DNA

<213> Homo sapiens

<220>

<221> intron

<222> (8)..(14)

<223> First 7 base of Intron 2

<400> 14

actccaggtg agcg

14

<210> 15

<211> 14

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (1)..(7)

<223> Wherein N is any nucleotide

<220>

<221> intron

<222> (1)..(7)

<223> Last 7 bases of Intron 2

<400> 15

nnnnnnncta tgcc

14

<210> 16

<211> 173

<212> DNA

<213> Homo sapiens

<220>
 <221> intron
 <222> (8)..(166)
 <223> Full Sequence of Intron 3

<400> 16
 aacgcagccg aagaaaacat ttctgtcgtg actcctgcgg tgcttgggtc gggacagcca 60
 gagatggagc caccgcgag accgtcgggt gtgggcagct ttccggtgtc tcctgggagg 120
 ggagttgggc tgggcctgtg actcctcagc ctctgttttc cccagggat gtc 173

<210> 17
 <211> 46
 <212> PRT
 <213> Homo sapiens

<400> 17
 Thr Ala Ala Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly
 1 5 10 15
 Ser Gly Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly
 20 25 30
 Ser Phe Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
 35 40 45

<210> 18
 <211> 104
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Intron Y

<400> 18
 ggcctccccg gggtcggcgt ccggctgggg ttgagggcgg ccgggggggaa ccagcgacat 60
 gcggagagca gcgcaggcga ctcagggcgc ttcccccgca ggtg 104

<210> 19
 <211> 34
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Reding Frame One of Intron Y

<400> 19
 Gly Leu Pro Gly Val Gly Val Arg Leu Gly Leu Arg Ala Ala Gly Gly
 1 5 10 15
 Asn Gln Arg His Ala Glu Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro
 20 25 30
 Arg Arg

<210> 20
<211> 10
<212> PRT
<213> Homo sapiens

<220>
<223> Reading Frame Two of Intron Y before termination
Codon

<400> 20
Ala Ser Pro Gly Ser Ala Ser Gly Trp Gly
1 5 10

<210> 21
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<223> Reading Frame Two of Intron Y after termination
Codon

D10
<400> 21
Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
1 5 10 15

Gln Gly Ala Ser Pro Ala Gly
20

<210> 22
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<223> Reading Frame Three of Intron Y

<400> 22
Pro Pro Arg Gly Arg Arg Pro Ala Gly Val Glu Gly Gly Arg Gly Glu
1 5 10 15

Pro Ala Thr Cys Gly Glu Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro
20 25 30

Gln Val

<210> 23
<211> 38
<212> DNA
<213> Homo sapiens

<220>
<223> Intron 1

<400> 23
gtggctgtgc tttggttttaa cttccttttt aaccagaa

38

<210> 24
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<223> Intron 1 Translation

<400> 24
Val Ala Val Leu Trp Phe Asn Phe Leu Phe Asn Gln Lys
1 5 10

<210> 25
<211> 36
<212> DNA
<213> Homo sapiens

<220>
<223> Intron Alpha

D10 <400> 25
gtggatgtga cgggcgcgta cgacaccatc cccag

36

<210> 26
<211> 12
<212> PRT
<213> Homo sapiens

<220>
<223> Intron Alpha Translation

<400> 26
Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln
1 5 10

<210> 27
<211> 182
<212> DNA
<213> Homo sapiens

<220>
<223> Intron Beta

<400> 27
gtctctacct tgacagacct ccagccgtac atgcgacagt tcgtggctca cctgcaggag 60
accagcccgc tgagggatgc cgtcgtcatc gagcagagct cctccctgaa tgaggccagc 120
agtggcctct tcgacgtctt cctacgcttc atgtgccacc acgccgtgcg catcaggggc 180
aa 182

<210> 28
<211> 61
<212> PRT
<213> Homo sapiens

<220>

<223> Intron Beta Translation

<400> 28

Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
1 5 10 15

His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln
20 25 30

Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu
35 40 45

Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys
50 55 60

<210> 29

<211> 226

<212> DNA

<213> Homo sapiens

<220>

<223> Intron 2

<400> 29

gtgagcgac ctggccggaa gtggagcctg tgccccggctg gggcaggtgc tgctgcaggg 60
ccgttgcgtc cacctctgct tccgtgtggg gcaggcgact gccaatccca aagggtcaga 120
tgccacaggg tgcccctcgt cccatctggg gctgagcaca aatgcatttt tctgtgggag 180
tgaggggtgcc tcacaacggg agcagttttc tgtgctattt tggttaa 226

<210> 30

<211> 159

<212> DNA

<213> Homo sapiens

<220>

<223> Intron 3

<400> 30

ccgaagaaaa catttctgtc gtgactcctg cgggtgcttgg gtcgggacag ccagagatgg 60
agccaccccg cagaccgtcg ggtgtgggca gctttccggg gtctcctggg aggggagttg 120
ggctgggacct gtgactctc agcctctggt ttccccag 159

<210> 31

<211> 44

<212> PRT

<213> Homo sapiens

<220>

<223> Intron 3 Translation

<400> 31

Ala Glu Glu Asn Ile Ser Val Val Thr Pro Ala Val Leu Gly Ser Gly
1 5 10 15

Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe

Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
 35 40

<210> 32
 <211> 262
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Intron X. Complete length unknown

<400> 32
 gacagtcacc agggggggttg accgccggac tgggcgtccc caggggttgac tataggacca 60
 ggtgtccagg tgccctgcaa gtagaggggc tctcagaggc gtctggctgg catgggtgga 120
 cgtggccccc ggcatggcct tctgcgtgtg ctgccgtggg tgccctgagc cctcactgag 180
 tcgggtggggg cttgtggcct cccgtgagct tccccctagt ctgttgtctg gctgagcaag 240
 cctcctgagg ggctctctat tg 262

<210> 33
 <211> 218
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Partial Sequence of Genomic Intron (approximately
 2.7 kb)

<400> 33
 gtggctgtgc tttggtttaa cttccttttt aaccagaagt gcgtttgagc cccacatttg 60
 gtatcagctt agatgaaggg ccgggaggag gggccacggg acacagccag ggccatggca 120
 cggcgccccc ccatttgtgc gcacagttag gtggccgagg tgccgggtgcc tccagaaaag 180
 cagcgtgggg gtgtaggggg agctcctggg gcagggac 218

<210> 34
 <211> 2031
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (1767)..(1769)
 <223> Wherein N is A, C, G or T

<220>
 <223> N-Terminal Truncated Telomerase

<400> 34
 atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
 gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
 cgcggggacc cggcggcttt ccgcgcgctg gtggccaggt gcctggtgtg cgtgccctgg 180
 gacgcacggc cgccccccgc cgccccctcc ttccgccagg tgtcctgcct gaaggagctg 240
 gtggcccgag tgctgcagag gctgtgcgag cgcggcgcga agaactgtgt ggccttcggc 300
 ttcgcgctgc tggacggggc ccgcgggggc ccccccgagg ccttcaccac cagcgtgcgc 360
 agctacctgc ccaacacggt gaccgacgca ctgcggggga gcggggcgtg ggggctgctg 420
 ctgcgcgcgc tgggcgacga cgtgctggtt cacctgctgg cacgctgcgc gctctttgtg 480

ctggtggctc ccagctgagc ctaccaggtg tgcggggccg cgctgtacca gctcggcgct 540
 gccactcagg cccggccccc gccacacgct agtggacccc gaaggcgtct gggatgcgaa 600
 cgggcctgga accatagcgt cagggaggcc ggggtccccc tgggcctgcc agccccgggt 660
 gcgaggaggc gcgggggagc tgcagccga agtctgccgt tgcccaagag gccaggcgt 720
 ggcgctgccc ctgagccgga gcggacgccc gttgggcagg ggtcctgggc ccaccgggc 780
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 gaggacacag acccccgtcg cctggtgcag ctgctccgcc agcacagcag cccctggcag 1380
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 gccaaagtct cgctgcagga gctgacgtgg aagatgagcg tgcgggactg cgcttggtcg 1560
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 ctgagaggcg tctggctggc atgggtggac gtggccccgg gcatggcctt ctgcgtgtgc 1920
 tgccgtgggt gccctgagcc ctactgagt cgggtggggc ttgtggcttc ccgtgagctt 1980
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<210> 35
 <211> 588
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Protein Predicted by SEQ ID NO:34

<400> 35

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
 85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
 100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr

115 120 125
 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
 130 135 140
 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
 145 150 155 160
 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
 165 170 175
 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430

Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly
 580 585

<210> 36
 <211> 2041
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Truncated Protein 1; Intron 1 Addition

<400> 36
 atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
 gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
 cgcggggacc cggcggcgtt ccgcgcgctg gtggccaggt gcctggtgtg cgtgccctgg 180
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 ttgcgcgtgc tggacggggc ccgcgggggc ccccccgagg ccttcaccac cagcgtgcgc 360
 agctacctgc ccaacacggt gaccgacgca ctgcggggga gcggggcgct ggggctgctg 420
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 ctggtggctc ccagctgcgc ctaccaggtg tcggggccgc cgctgtacca gctcggcgct 540
 gccactcagg cccggcccc gccacacgct agtggacccc gaaggcgtct gggatgcgaa 600
 cgggcctgga accatagcgt cagggaggcc ggggtcccc tgggcctgcc agccccgggt 660
 gcgaggaggc gcgggggcag tgccagccga agtctgccgt tgcccaagag gcccaggcgt 720
 ggcgctgccc ctgagccgga gcggacgccc gttgggcagg ggtcctgggc ccaccgggc 780
 aggacgcgtg gaccgagtga ccgtggtttc tgtgtggtgt cactgccag acccgccgaa 840
 gaagccacct ctttggaggg tgcgtctctt ggcacgcgcc actcccaccc atcgtgggc 900
 cgccagcacc acgcgggccc cccatccaca tcgcggccac cagtcacctg ggacacgcct 960
 tgtcccccg tgtacgccga gaccaagcac ttctctact cctcaggcga caaggagcag 1020

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gtggagacca tctttctggg ttccaggccc tggatgccag ggactccccg cagggtgccc 1140
cgcctgcccc agcgctactg gcaaagtgcg cccctgtttc tggagctgct tgggaaccac 1200
gcgcagtgcc cctacggggt gctcctcaag acgcactgcc cgctgcgagc tgcggtcacc 1260
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ctgtcgggaag cagaggtcag gcagcatcgg gaagccaggc ccgccctgct gacgtccaga 1860
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a
2041

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<210> 37
 <211> 670
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein 1; Encoded by SEQ ID NO:36

D10

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<400> 37
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
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His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
  20           25           30
Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
  35           40           45
Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
  50           55           60
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
  65           70           75           80
Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
  85           90           95
Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
  100          105          110
Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
  115          120          125
Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
  130          135          140
Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
  145          150          155          160

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Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
 165 170 175
 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser

465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
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 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
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 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu Trp Phe
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 Thr Phe Leu Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly
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<210> 38

<211> 2541

<212> DNA

<213> Homo sapiens

<220>

<223> Truncated Protein 2; Alpha Intron Addition

<400> 38

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 <213> Homo sapiens

<220>
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 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
 85 90 95
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
 100 105 110
 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
 115 120 125
 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
 130 135 140
 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
 145 150 155 160
 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
 165 170 175
 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His

385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
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 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
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 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
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 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700

D10

Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro Val Pro
 755 760 765
 Gly Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val
 770 775 780
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 Ala Ala Pro Ala Phe Val Gly
 805

D10
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 <211> 3396
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Reference Telomerase; with Intron Alpha and Beta

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D10

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<210> 41

<211> 3069

<212> DNA

<213> Homo sapiens

<220>

<223> Truncated Protein 3; with Introns Alpha, Beta and
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<400> 41

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<210> 42

<211> 948

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 3; Encoded by SEQ ID NO:41

<400> 42

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 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65 70 75 80
 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
 85 90 95
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
 100 105 110
 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
 115 120 125
 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
 130 135 140
 Glu Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
 145 150 155 160
 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
 165 170 175
 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
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 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln

370

375

380

Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
385 390 395 400

Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
405 410 415

Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
420 425 430

Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
435 440 445

Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
450 455 460

Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
465 470 475 480

Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
485 490 495

Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
500 505 510

Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
515 520 525

Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
530 535 540

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
545 550 555 560

Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
565 570 575

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
580 585 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
595 600 605

His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
625 630 635 640

Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
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Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
660 665 670

Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
675 680 685

D10

Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
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 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
 755 760 765
 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
 770 775 780
 Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
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 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
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 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
 835 840 845
 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
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 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
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 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
 885 890 895
 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
 900 905 910
 Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
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 Asp Tyr Ser Arg
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<210> 43
 <211> 3362
 <212> DNA
 <213> Homo sapiens

<220>

<223> Altered C-terminus Protein; with Intron Alpha,
Beta and 3

<400> 43

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 ga 3362

<210> 44
 <211> 1096
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Altered C-terminus Protein; Encoded by SEQ ID
 NO:43

<400> 44

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 His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65 70 75 80
 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
 85 90 95
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
 100 105 110
 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
 115 120 125
 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
 130 135 140
 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
 145 150 155 160
 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
 165 170 175
 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg

225
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 230 235 240 255
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
 755 760 765
 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
 770 775 780
 Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
 785 790 795 800
 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
 805 810 815
 Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
 820 825 830
 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
 835 840 845

Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
 850 855 860
 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
 865 870 875 880
 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
 885 890 895
 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
 900 905 910
 Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
 915 920 925
 Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
 930 935 940
 Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
 945 950 955 960
 Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
 965 970 975
 Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
 980 985 990
 Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
 995 1000 1005
 Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
 1010 1015 1020
 Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
 1025 1030 1035 1040
 Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu Glu Asn
 1045 1050 1055
 Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro Glu Met
 1060 1065 1070
 Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val Ser Pro
 1075 1080 1085
 Gly Arg Gly Val Gly Leu Gly Leu
 1090 1095

<210> 45

<211> 3918

<212> DNA

<213> Homo sapiens

<220>

<223> Protein that lacks Motif A; with Intron Beta

<400> 45

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tgagtttttc agttttga                                     3918

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<210> 46
<211> 1120
<212> PRT
<213> Homo sapiens

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<220>
<223> Protein that lacks Motif A; Encoded by SEQ ID
      NO:45

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D18

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<400> 46
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His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
      20              25              30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
      35              40              45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
      50              55              60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
      65              70              75              80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
      85              90              95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
      100              105              110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
      115              120              125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
      130              135              140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
      145              150              155              160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
      165              170              175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
      180              185              190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
      195              200              205

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Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
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 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
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 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
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 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
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 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
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 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
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 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
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 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys

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 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
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 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
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 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
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 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile
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 Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser
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 770 775 780
 Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe
 785 790 795 800
 Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys
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 Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu
 820 825 830

Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp
835 840 845

Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His
850 855 860

Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro
865 870 875 880

Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro
885 890 895

Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala
900 905 910

His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu
915 920 925

Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala
930 935 940

Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg
945 950 955 960

Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp
965 970 975

Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile
980 985 990

Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro
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Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile
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Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala
1025 1030 1035 1040

Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu
1045 1050 1055

Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg
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His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln
1075 1080 1085

Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu
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Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
1105 1110 1115 1120

<210> 47
 <211> 3033
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Truncated Protein that lacks Motif A; with Introns
 Beta and 2

<400> 47

D10

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 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein that lacks Motif A; Encoded by
 SEQ ID NO:47

<400> 48
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His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
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Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
 85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
 100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
 115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
 130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
 145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
 165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile
 705 710 715 720
 Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln
 725 730 735
 Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser
 740 745 750
 Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu
 755 760 765
 Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser
 770 775 780
 Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe
 785 790 795 800
 Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys
 805 810 815
 Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu
 820 825 830
 Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp
 835 840 845

D10

Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His
850 855 860

Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro
865 870 875 880

Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro
885 890 895

Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala
900 905 910

His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu
915 920 925

Glu Val Gln Ser Asp Tyr Ser Arg
930 935

<210> 49
<211> 3326
<212> DNA
<213> Homo sapiens

<220>
<223> Protein Lacking Motif A and Altered C-Terminus;
with Introns Beta and 3

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<211> 1084

<212> PRT

<213> Homo sapiens

<220>

<223> Protein Lacking Motif A and Altered C-Terminus;
Encoded by SEQ ID NO:49

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His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
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Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
 115 120 125
 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
 130 135 140
 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
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 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
 165 170 175
 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
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 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415

D18

Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
420 425 430

Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
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Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
450 455 460

Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
465 470 475 480

Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
485 490 495

Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
500 505 510

Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
515 520 525

Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
530 535 540

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
545 550 555 560

Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
565 570 575

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
580 585 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
595 600 605

His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
625 630 635 640

Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
645 650 655

Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
660 665 670

Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
675 680 685

Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
690 695 700

Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile
705 710 715 720

Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln

725										730					735				
Lys	Ala	Ala	His	Gly	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser				
			740						745					750					
Thr	Leu	Thr	Asp	Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu				
		755					760					765							
Gln	Glu	Thr	Ser	Pro	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser				
	770					775					780								
Ser	Leu	Asn	Glu	Ala	Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	Arg	Phe				
785					790					795					800				
Met	Cys	His	His	Ala	Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val	Gln	Cys				
				805					810					815					
Gln	Gly	Ile	Pro	Gln	Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu				
		820						825					830						
Cys	Tyr	Gly	Asp	Met	Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp				
	835						840						845						
Gly	Leu	Leu	Leu	Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His				
	850					855						860							
Leu	Thr	His	Ala	Lys	Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro				
865					870					875					880				
Glu	Tyr	Gly	Cys	Val	Val	Asn	Leu	Arg	Lys	Thr	Val	Val	Asn	Phe	Pro				
			885						890					895					
Val	Glu	Asp	Glu	Ala	Leu	Gly	Gly	Thr	Ala	Phe	Val	Gln	Met	Pro	Ala				
		900						905					910						
His	Gly	Leu	Phe	Pro	Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	Thr	Leu				
	915						920					925							
Glu	Val	Gln	Ser	Asp	Tyr	Ser	Ser	Tyr	Ala	Arg	Thr	Ser	Ile	Arg	Ala				
	930					935					940								
Ser	Leu	Thr	Phe	Asn	Arg	Gly	Phe	Lys	Ala	Gly	Arg	Asn	Met	Arg	Arg				
945				950						955					960				
Lys	Leu	Phe	Gly	Val	Leu	Arg	Leu	Lys	Cys	His	Ser	Leu	Phe	Leu	Asp				
			965						970					975					
Leu	Gln	Val	Asn	Ser	Leu	Gln	Thr	Val	Cys	Thr	Asn	Ile	Tyr	Lys	Ile				
		980						985					990						
Leu	Leu	Leu	Gln	Ala	Tyr	Arg	Phe	His	Ala	Cys	Val	Leu	Gln	Leu	Pro				
	995					1000							1005						
Phe	His	Gln	Gln	Val	Trp	Lys	Asn	Pro	Thr	Phe	Phe	Leu	Arg	Val	Ile				
	1010					1015					1020								
Ser	Asp	Thr	Ala	Ser	Leu	Cys	Tyr	Ser	Ile	Leu	Lys	Ala	Lys	Asn	Ala				
1025				1030						1035					1040				

Glu Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly
 1045 1050 1055

Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe
 1060 1065 1070

Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
 1075 1080

<210> 51
 <211> 2135
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (1871)..(1873)
 <223> Wherein N is A, C, G or T

<220>
 <223> N-Terminal Truncated Telomerase (ver. 2); with
 Intron Y

<400> 51
 atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
 gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctgggtgcag 120
 cgcgggggacc cggcggtttt ccgcgcgctg gtggccagc gcctgggtgtg cgtgcccttg 180
 gacgcacggc cgccccccgc cgccccctcc ttccgccagg tgggcctccc cggggtcggc 240
 gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgaggc 300
 gactcagggc gcttcccccg caggtgtcct gcctgaagga gctgggtggc cgagtgtgc 360
 agaggctgtg cgagcgcggc gcgaagaacg tgctggcctt cggcttcgcg ctgctggacg 420
 gggcccgcg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaca 480
 cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgtgtgcg cgcgtgggcg 540
 acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgtgtgtg gctcccagct 600
 gcgcctacca ggtgtgcggg ccgcgcgtgt accagctcgg cgctgccact caggcccggc 660
 ccccgccaca cgctagtggc ccccgaggc gtctgggatg cgaacggggc tggaaccata 720
 gcgtcaggga ggccggggtc cccctgggccc tgccagcccc ggggtgcgagg aggcgcgggg 780
 gcagtgccag ccgaagtctg ccgttgcccc agagggcccag gcgtggcgct gcccctgagc 840
 cggagcggac gcccggttggg caggggtcct gggccccacc gggcaggacg cgtggaccgc 900
 gtgaccgtgg tttctgtgtg gtgtcacctg ccagacccgc cgaagaagcc acctctttgg 960
 aggggtgcgt ctctggcacg cgcactccc acccatccgt gggccgccag caccacgcgg 1020
 gccccccatc cacatcgcgg ccaccacgtc cctgggacac gccttgtccc ccggtgtacg 1080
 ccgagaccaa gcacttcctc tactcctcag gcgacaagga gcagctgcgg cctccttcc 1140
 tactcagctc tctgaggccc agcctgactg gcgctcggag gctcgtggag accatcttcc 1200
 tgggttccag gccctggatg ccagggaact cccgcagggt gcccgcctg cccagcgct 1260
 actggcaaat gcggccctg tttctggagc tgcttgggaa ccacgcgcag tgcccctacg 1320
 ggggtgctct caagacgcac tgcccgtgc gagctgcggt caccacagca gccggtgtct 1380
 gtgcccggga gaagccccag ggctctgtgg cggccccga ggaggaggac acagaccccc 1440
 gtcgcctggt gcagctgtc cgccagcaca cgagccccg gcaggtgtac ggctcgtgc 1500
 gggcctgcct gcgcgggctg gtgccccag gcctctgggg ctccaggcac aacgaacgcc 1560
 gcttcctcag gaacaccaag aagttcatct cctggggaa gcatgccaa ctctcgtgc 1620
 aggagctgac gtggaagatg agcgtgcggg actgcgctt gctgcgcagg agcccagggg 1680
 ttggctgtgt tccggccgca gagcaccgtc tgcgtgagga gatcctggcc aagttcctgc 1740
 actggctgat gagtgtgtac gtcgtcgagc tgctcaggtc tttcttttat gtcacggaga 1800
 ccacgtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaaa 1860
 gcattggaat nnnagacgtc accagggggg ttgaccgcgc gactgggcgt cccaggggtt 1920

gactatagga ccagggtgtcc aggtgccctg caagtagagg ggctctcaga ggcgtctggc 1980
 tggcatgggt ggacgtggcc ccgggcatgg ccttctgcgt gtgctgccgt ggggtgccctg 2040
 agccctcact gagtcggtgg gggcttgtgg cttcccgta gcttccccct agtctgttgt 2100
 ctggctgagc aagcctcctg aggggctctc tattg 2135

<210> 52
 <211> 622
 <212> PRT
 <213> Homo sapiens

<220>
 <223> N-Terminal Truncated Telomerase (ver.2); encoded
 by SEQ ID NO:51 and ORF1 of Intron Y

<400> 52
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
 65 70 75 80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
 85 90 95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
 100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser

225 230 235 240
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 D10 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly
610 615 620

<210> 53

<211> 84

<212> PRT

<213> Homo sapiens

<220>

D10
<223> Splicing Variant of Human Telomerase encoded by
Intron Y, ORF2, before the termination codon.
SEQ ID NOS: 51,55,59,63,67,71,75,79,83 encode this
fragment

<400> 53

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ala Ser Pro Gly Ser Ala
65 70 75 80

Ser Gly Trp Gly

<210> 54

<211> 537

<212> PRT

<213> Homo sapiens

<220>

<223> N-Terminal Truncated Telomerase (ver. 2); encoded
by SEQ ID NO:51, with Y intron, ORF2, after the
termination codon

<400> 54

Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro His Ala Ser Gly Pro Arg Arg
130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
165 170 175

Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
180 185 190

Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
195 200 205

Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
210 215 220

Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
225 230 235 240

Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
245 250 255

Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
260 265 270

Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
275 280 285

Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
290 295 300

Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
305 310 315 320

Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
325 330 335

Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
340 345 350

Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
355 360 365

Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
370 375 380

Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
385 390 395 400

Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
405 410 415

Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
420 425 430

Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
435 440 445

His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
450 455 460

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
465 470 475 480

Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
485 490 495

Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
500 505 510

Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
515 520 525

Val Trp Ser Lys Leu Gln Ser Ile Gly
530 535

<210> 55

<211> 2145

<212> DNA

<213> Homo sapiens

<220>

<223> Truncated Protein 1 (ver.2); with Introns Y and 1

<400> 55

atgccgcgcg ctcgccgctg ccgagccgctg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggccccc agggctggcg gctggtgcag 120
cgcggggacc cggcggtttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180

gacgcacggc cgccccccgc cgccccctcc ttccgccagg tgggcctccc cggggtcggc 240
 gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgaggc 300
 gactcagggc gcttcccccg caggtgtcct gcctgaagga gctgggtggc cgagtgtgc 360
 agaggctgtg cgagcgcggc gcgaagaacg tgctggcctt cggcttcgcg ctgctggacg 420
 gggcccgcg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaca 480
 cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtgggcg 540
 acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600
 gcgcctacca ggtgtgcggg ccgccgctgt accagctcgg cgtgcact caggcccggc 660
 ccccgccaca cgctagtga cccgaaggc gtctgggatg cgaacggggc tggaaccata 720
 gcgtcagggg ggcgggggtc cccctggggc tggcagcccc ggggtgcgagg aggcgcgggg 780
 gcagtgccag ccgaagtctg ccgttgccca agaggccag gcgtggcgct gcccctgagc 840
 cggagcggac gcccgttggg caggggtcct gggccacccc gggcaggacg cgtggaccga 900
 gtgacgtgg tttctgtgtg gtgtcacctg ccagaccgc cgaagaagcc acctctttgg 960
 aggggtgcgt ctctggcacg cgccactccc acccatccgt gggccggcag caccacgcgg 1020
 gccccccatc cacatcgcg ccaccacgtc cctgggacac gccttgtccc ccggtgtacg 1080
 ccgagaccaa gcacttcctc tactcctcag gcgacaagga gcagctgcgg cctccttccc 1140
 tactcagctc tctgaggccc agcctgactg gcgctcggag gctcgtggag acctcctttc 1200
 tgggttccag gccctggatg ccagggactc cccgcaggtt gccccgcctg cccagcgct 1260
 actggcaaat gcggccctg tttctggagc tgcttgggaa ccacgcgcag tgcccctacg 1320
 ggggtgtcct caagacgcac tgcccgtgc gagctgcggt caccagca gccggtgtct 1380
 gtgcccggga gaagccccag ggctctgtgg cggccccga ggaggaggac acagaccccc 1440
 gtgcctgggt gcagctgctc cgccagcaca gcagccctg gcaggtgtac ggcttcgtgc 1500
 gggcctgcct gcgcggctg gtgccccag ccctctgggg ctccaggcac aacgaacgcc 1560
 gcttcctcag gaacaccaag aagttcatct ccctgggaa gcatgccaag ctctcgctgc 1620
 aggagctgac gtggaagatg agcgtgcggg actgcgcttg gctgcgcagg agcccagggg 1680
 ttggctgtgt tccggccgca gagcaccgtc tgctgagga gatcctggcc aagttcctgc 1740
 actggctgat gagtgtgtac gtgctcgagc tgctcaggtc tttcttttat gtcacggaga 1800
 ccacgtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaaa 1860
 gcattggaat cagacagcac ttgaagaggg tgcagctgcg ggagctgtcg gaagcagagg 1920
 tcaggcagca tcgggaagcc agggccgccc tgctgacgtc cagactccgc ttcaccccca 1980
 agcctgacgg gctgcggccg attgtgaaca tggactacgt cgtgggagcc agaacgttcc 2040
 gcagagaaaa gaggggtggt gtgctttggt ttaacttct ttttaaccag aagccgagcg 2100
 tctcacctcg aggggtgaagg cactgttcag cgtgctcaac tacga 2145

<210> 56
 <211> 704
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein 1 (ver.2); encoded by SEQ ID
 NO:55, with Y Intron ORF1

<400> 56
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15
 His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
 65 70 75 80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
 85 90 95
 Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
 100 105 110
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165 170 175
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu
 675 680 685
 Trp Phe Thr Phe Leu Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly

690

695

700

<210> 57
 <211> 619
 <212> PRT
 <213> Homo sapiens

<220>

<223> Truncated Protein 1 (ver.2): encoded by SEQ ID
 NO:55, with Intron Y ORF2 after the termination
 codon

<400> 57

Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
 1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
 20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
 35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
 50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
 100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
 115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
 130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
 145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
 165 170 175

Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
 180 185 190

Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
 195 200 205

Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
 210 215 220

D12

Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
 225 230 235 240
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
 245 250 255
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
 260 265 270
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
 275 280 285
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
 290 295 300
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
 305 310 315 320
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
 325 330 335
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
 340 345 350
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
 355 360 365
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
 370 375 380
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
 385 390 395 400
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
 405 410 415
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
 420 425 430
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
 435 440 445
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
 450 455 460
 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
 465 470 475 480
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
 485 490 495
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
 500 505 510
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
 515 520 525

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
530 535 540

Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
545 550 555 560

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
565 570 575

Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
580 585 590

Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu Trp Phe Thr Phe Leu
595 600 605

Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly
610 615

<210> 58

<211> 704

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 1 (ver.2); encoded by SEQ ID
NO:55, with Intron Y ORF3

<400> 58

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
65 70 75 80

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
85 90 95

Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165 170 175
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460

D18

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu
 675 680 685
 Trp Phe Thr Phe Leu Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly
 690 695 700

<210> 59

<211> 2645

<212> DNA

<213> Homo sapiens

<220>

<223> Truncated Protein 2 (ver.2); with Intron Y and Alpha

<400> 59

atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
cgcggggacc cggcggtttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
gacgcacggc cgccccccgc cgccccctcc ttccgccagg tgggcctccc cggggtcggc 240
gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgaggc 300
gactcagggc gcttcccccg caggtgtcct gcctgaagga gctggtggcc cgagtgtgc 360
agaggctgtg cgagcgcggc gcgaagaacg tgctggcctt cggtctcgcg ctgctggacg 420
gggcccgcgg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaca 480
cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtggcg 540
acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600
gcgcctacca ggtgtgcggg ccgccgctgt accagctcgg cgtgccact caggcccggc 660
ccccgccaca cgctagtggg cccgaaggc gtctgggatg cgaacggggc tggaaaccata 720
gcgtcagggg ggcgggggtc cccctggggc tgccagcccc ggggtgcgagg aggcgcgggg 780
gcagtgccag ccgaagtctg ccgttgccca agaggcccag gcgtggcgct gccctgagc 840
cggagcggac gcccggttggg caggggtcct gggcccaccc gggcaggacg cgtggaccga 900
gtgaccgtgg tttctgtgtg gtgtcacctg ccagaccgc cgaagaagcc acctctttgg 960
aggggtgcgt ctctggcacg cgccactccc acccatccgt gggccgccag caccacgcgg 1020
gccccccat cacatcgcg ccaccacgtc cctgggacac gccttgtccc ccggtgtacg 1080
ccgagaccaa gcacttctc tactctcag gcgacaagga gcagtgcgg ccctccttcc 1140
tactcagctc tctgaggccc agcctgactg gctcgtggag gctcgtggag acctcttcc 1200
tgggttccag gccctggatg ccagggactc ccgcaggtt gccccgcctg cccagcgct 1260
actggcaaat gcggccctg tttctggagc tgcttgggaa ccacgcgcag tgcccctacg 1320
gggtgctcct caagacgcac tgcccgtgc gagctgcggt caccacagca gccggtgtct 1380
gtgcccggga gaagccccag ggctctgtgg cggccccga ggaggaggac acagaccccc 1440
gtgcctggt gcagctgtc cgccagcaca gcagcccctg gcaggtgtac ggcttcgtgc 1500
gggcctgcct gcgcgggtg gtgccccag gcctctgggg ctccaggcac aacgaacgcc 1560
gcttctcag gaacaccaag aagttcatct ccctggggaa gcatgccaag ctctcgctgc 1620
aggagctgac gtggaagatg agcgtgcggg actgcgctt gctgcgcagg agcccagggg 1680
ttggctgtgt tccggccgca gagcaccgtc tgcgtgagga gatcctggcc aagttcctgc 1740
actggtgat gagtgtgtac gtctcgagc tctcaggtc tttcttttat gtcacggaga 1800
ccacgtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaaa 1860
gcattggaat cagacagcac ttgaagaggg tgcagctgcg ggagctgtcg gaagcagagg 1920
tcaggcagca tcgggaagcc agggccgccc tgctgacgtc cagactccgc ttcacccca 1980
agcctgacgg gctgcggccg attgtgaaca tggactacgt cgtgggagcc agaacgttcc 2040
gcagagaaaa gagggccgag cgtctcacct cgagggtgaa ggcactgttc agcgtgtca 2100
actacgagcg ggcgcggcgc cccggcctcc tgggcgcctc tgtgctgggc ctggacgata 2160
tccacagggc ctggcgacac ttctgtgtgc gtgtgcgggc ccaggaccgc ccgcctgagc 2220
tgtactttgt caaggtggat gtgacgggcg cgtacgacac catccccag gacaggctca 2280
cggaggtcat cgccagcatc atcaaacccc agaacacgta ctgctgctc cggatgccg 2340
tggtcagaa ggccgcccac gggcacgtcc gcaaggcctt caagagccac gtcctacgtc 2400
cagtgccagg ggatcccga gggctccatc ctctccacgc tgctctgcag cctgtgtac 2460
ggcgacatgg agaacaagct gtttgcgggg attcggcggg acgggctgct cctgcgtttg 2520
gtggatgatt tcttgttggg gacacctcac ctacccacg cgaaaaacct cctcaggacc 2580
ctggtccgag gtgtccctga gtatggctgc gtggtgaact tgcggaagac agtgggtgaac 2640
ttccc 2645

<210> 60

<211> 841

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 2 (ver.2); encoded by SEQ ID
NO:59, with Intron Y ORF1

<400> 60

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
340 345 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
355 360 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
370 375 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
385 390 395 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
405 410 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
420 425 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
450 455 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
465 470 475 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
485 490 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
500 505 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
530 535 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
610 615 620

Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
625 630 635 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
645 650 655

Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
660 665 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
675 680 685

Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
690 695 700

Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
705 710 715 720

His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
725 730 735

Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
740 745 750

Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
755 760 765

Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
770 775 780

Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro
785 790 795 800

Val Pro Gly Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln
805 810 815

Pro Val Leu Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala
820 825 830

Gly Arg Ala Ala Pro Ala Phe Val Gly
835 840

<210> 61

<211> 756

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 2 (ver.2); encoded by SEQ ID
NO:59 with Intron Y ORF2 after the termination
codon

<400> 61

Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg

20 25 30
 Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
 35 40 45
 Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
 50 55 60
 Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
 65 70 75 80
 Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
 85 90 95
 Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
 100 105 110
 Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
 115 120 125
 Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
 130 135 140
 Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
 145 150 155 160
 Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
 165 170 175
 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
 180 185 190
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
 195 200 205
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
 210 215 220
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
 225 230 235 240
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
 245 250 255
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
 260 265 270
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
 275 280 285
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
 290 295 300
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
 305 310 315 320
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
 325 330 335

D10

Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
 340 345 350

Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
 355 360 365

Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
 370 375 380

Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
 385 390 395 400

Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
 405 410 415

Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
 420 425 430

Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
 435 440 445

His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
 450 455 460

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
 465 470 475 480

Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
 485 490 495

Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
 500 505 510

Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
 515 520 525

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
 530 535 540

Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
 545 550 555 560

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
 565 570 575

Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
 580 585 590

Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
 595 600 605

Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
 610 615 620

Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
 625 630 635 640

Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr
645 650 655

Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp
660 665 670

Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr
675 680 685

Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val
690 695 700

Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro Val Pro Gly Asp Pro
705 710 715 720

Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu Arg Arg
725 730 735

His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala Ala Pro
740 745 750

Ala Phe Val Gly
755

<210> 62

<211> 841

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 2 (ver.2); encoded by SEQ ID NO:
59 with Intron Y ORF3

<400> 62

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
65 70 75 80

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
85 90 95

Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165 170 175
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430

D10

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp

740 745 750
 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
 755 760 765
 Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
 770 775 780
 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro
 785 790 795 800
 Val Pro Gly Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln
 805 810 815
 Pro Val Leu Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala
 820 825 830
 Gly Arg Ala Ala Pro Ala Phe Val Gly
 835 840

<210> 63
 <211> 3500
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Reference Protein (ver.2); with Introns Y, Alpha
 and Beta

<400> 63
 atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
 gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctgggtgcag 120
 cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctgggtgtg cgtgccctgg 180
 gacgcacggc cccccccgc cgccccctcc ttccgccagg tgggcctccc cggggtcggc 240
 gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
 gactcagggc gcttcccccg caggtgtcct gcctgaagga gctgggtggc cgagtgtgc 360
 agaggctgtg cgagcgcggc gcgaagaacg tgctggcctt cggcttcgcg ctgctggacg 420
 gggccgcggc gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccacaa 480
 cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgttgccg cgcgtgggcg 540
 acgacgtgct ggttcacctg ctggcacgct cgcgctctt tgtgctgggt gctcccagct 600
 gcgcctacca ggtgtgcggc ccgcgcgtgt accagctcgg cgctgccact caggcccggc 660
 ccccgccaca cgctagtggc cccgaaggc gtctgggatg cgaacggggc tggaaccata 720
 gcgtcagggc ggccggggtc cccctgggccc tgccagcccc ggggtgcgagg aggcgcgggg 780
 gcagtgccag ccgaagtctg ccgttgccca agaggcccag gcgtggcgct gccctgagc 840
 cggagcggac gcccggttgg caggggtcct gggcccaccc gggcaggacg cgtggaccga 900
 gtgaccgtgg tttctgtgtg gtgtcacctg ccagaccgcg cgaagaagcc acctctttgg 960
 aggggtgcgt ctctggcacg cgccactccc acccatccgt gggccgccag caccacgcgg 1020
 gcccccatc cacatcgcg ccaccacgtc cctgggacac gccttgtccc ccggtgtacg 1080
 ccgagaccaa gcacttcctc tactcctcag gcgacaagga gcagctgcgg cctccttcc 1140
 tactcagctc tctgaggccc agcctgactg gcgctcggag gctcgtggag accatcttc 1200
 tgggttccag gccctggatg ccagggaact cccgcagggt gcccgcctg cccagcgtc 1260
 actggcaaat gcggccctg tttctggagc tgcttgggaa ccacgcgcag tgcccctacg 1320
 ggggtgctct caagacgcac tgcccgtgc gagctgcggt caccacagca gccggtgtct 1380
 gtgcccggga gaagccccag ggctctgtgg cggcccccca ggaggaggac acagaccccc 1440
 gtcgcctggt gcagctgtc cgccagcaca gcagcccctg gcaggtgtac ggcttcgtgc 1500
 gggcctgcct gcgcggctg gtgccccag gcctctgggg ctccaggcac aacgaacgcc 1560
 gcttcctcag gaacaccaag aagttcatct ccctggggaa gcatgccaa gctcgcgtgc 1620

aggagctgac gtggaagatg agcgtgcggg gctgcgcttg gctgcgcagg agcccagggg 1680
 ttggtgtgt tccggccgca gagcaccgtc tgcgtgagga gatcctggcc aagttcctgc 1740
 actggctgat gagtgtgtac gtcgtcgagc tgctcaggtc tttcttttat gtcacggaga 1800
 ccacgtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaaa 1860
 gcattggaat cagacagcac ttgaagaggg tgcagctgcg ggagctgtcg gaagcagagg 1920
 tcaggcagca tcgggaagcc aggcccggcc tgctgacgtc cagactccgc ttcaccccca 1980
 agcctgacgg gctgcggccg attgtgaaca tggactacgt cgtgggagcc agaacgttcc 2040
 gcagagaaaa gagggccgag cgtctcacct cgagggtgaa ggcactgttc agcgtgtca 2100
 actacgagcg ggcgcgccgc cccggcctcc tgggcgcctc tgtgctgggc ctggacgata 2160
 tccacagggc ctggcgccacc ttcgtgctgc gtgtgcgggc ccaggaccgc ccgcctgagc 2220
 tgtactttgt caaggtggat gtgacgggcg cgtacgacac catccccag gacaggctca 2280
 cggaggtcat cgcacgcatc atcaaaccac agaacacgta ctgctgctgc cggatgccc 2340
 tgggtccagaa ggccgcccac gggcacgtcc gcaaggcctt caagagccac gtctctacct 2400
 tgacagacct ccagccgtac atgcgacagt tcgtggctca cctgcaggag accagccgc 2460
 tgagggatgc cgtcgtcatc gagcagagct cctccctgaa tgaggccagc agtggcctct 2520
 tcgacgtctt cctacgcttc atgtgccacc acgccgtgcg catcaggggc aagtcctacg 2580
 tccagtgccg ggggatcccg cagggtccca tctctccac gctgctctgc agcctgtgct 2640
 acggcgacat ggagaacaag ctgtttgcgg ggattcggcg ggacgggctg ctctgcgtt 2700
 tgggtgatga tttcttgtt gtgacacctc acctcaccca cgcgaaaacc tctctcagga 2760
 ccctgggtcg aggtgtccct gagtatggct gcgtgggtgaa cttgcggaag acagtgggtga 2820
 acttccctgt agaagacgag gccctgggtg gcacggcttt tgttcagatg ccggcccacg 2880
 gcctattccc ctggtgcggc ctgctgctgg ataccggac cctggagggtg cagagcgact 2940
 actccagcta tgcccgacc tccatcagag ccagtctcac cttcaaccgc ggcttcaagg 3000
 ctgggaggaa catgcgtcgc aaactctttg gggctctgcg gctgaagtgt cacagcctgt 3060
 ttctggattt gcaggtgaac agcctccaga cgggtgtgcac caacatctac aagatcctcc 3120
 tgctgcaggg gtacaggttt cagcatgtg tgctgcagct cccatttcat cagcaagttt 3180
 ggaagaaccc cacatttttc ctgcgcgtca tctctgacac ggcctccctc tgctactcca 3240
 tctgaaagc caagaacgca gggatgtcgc tgggggcca gggcgccgc ggccctctgc 3300
 cctccgaggg cgtgcagtgg ctgtgccacc aagcattcct gctcaagctg actcgacacc 3360
 gtgtcaccta cgtgccactc ctgggggtcac tcaggacagc ccagacgcag ctgagtcgga 3420
 agctcccggg gacgacgtg actgccctgg aggcgcagc caaccggca ctgccctcag 3480
 atttcaagac catcctggac 3500

<210> 64
 <211> 1165
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Reference Protein (ver.2); encoded by SEQ ID NO:63
 with Intron Y ORF1

<400> 64
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15
 His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
 65 70 75 80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
 85 90 95
 Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
 100 105 110
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165 170 175
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu

385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700

DR

Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
705 710 715 720

His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
725 730 735

Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
740 745 750

Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
755 760 765

Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
770 775 780

Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu
785 790 795 800

Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu
805 810 815

Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu
820 825 830

Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys
835 840 845

His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly
850 855 860

Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr
865 870 875 880

Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu
885 890 895

Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr
900 905 910

His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr
915 920 925

Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu
930 935 940

Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly
945 950 955 960

Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val
965 970 975

Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu
980 985 990

Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu
995 1000 1005

D10

Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln
1010 1015 1020

Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu
1025 1030 1035 1040

Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His
1045 1050 1055

Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp
1060 1065 1070

Thr Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser
1075 1080 1085

Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln
1090 1095 1100

Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val
1105 1110 1115 1120

Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu
1125 1130 1135

Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala
1140 1145 1150

Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
1155 1160 1165

<210> 65

<211> 1081

<212> PRT

<213> Homo sapiens

<220>

<223> Reference Protein (ver.2); encoded by SEQ ID NO:63
with Intron Y ORF2 after the termination codon

<400> 65

Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
 100 105 110
 Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
 115 120 125
 Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
 130 135 140
 Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
 145 150 155 160
 Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
 165 170 175
 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
 180 185 190
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
 195 200 205
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
 210 215 220
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
 225 230 235 240
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
 245 250 255
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
 260 265 270
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
 275 280 285
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
 290 295 300
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
 305 310 315 320
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
 325 330 335
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
 340 345 350
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
 355 360 365
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
 370 375 380
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
 385 390 395 400

D18

Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
405 410 415

Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
420 425 430

Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
435 440 445

His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
450 455 460

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
465 470 475 480

Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
485 490 495

Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
500 505 510

Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
515 520 525

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
530 535 540

Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
545 550 555 560

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
565 570 575

Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
580 585 590

Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
595 600 605

Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
610 615 620

Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
625 630 635 640

Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr
645 650 655

Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp
660 665 670

Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr
675 680 685

Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val
690 695 700

Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro

705 710 715 720
 Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg
 725 730 735
 Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser
 740 745 750
 Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg
 755 760 765
 Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser
 770 775 780
 Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn
 785 790 795 800
 Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val
 805 810 815
 Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe
 820 825 830
 Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn
 835 840 845
 Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly
 850 855 860
 Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys
 865 870 875 880
 Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser
 885 890 895
 Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly
 900 905 910
 Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg
 915 920 925
 Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln
 930 935 940
 Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr Arg
 945 950 955 960
 Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys
 965 970 975
 Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys
 980 985 990
 Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala Lys
 995 1000 1005
 Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys His
 1010 1015 1020

D10

Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val Pro
1025 1030 1035 1040

Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg Lys Leu
1045 1050 1055

Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro Ala Leu
1060 1065 1070

Pro Ser Asp Phe Lys Thr Ile Leu Asp
1075 1080

<210> 66

<211> 1165

<212> PRT

<213> Homo sapiens

<220>

<223> Reference Protein (ver.2); encoded by SEQ ID NO:63
with Intron Y ORF3

<400> 66

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
65 70 75 80

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
85 90 95

Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu

180 185 190
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495

D/O

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560 565
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
 740 745 750
 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
 755 760 765
 Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
 770 775 780
 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu
 785 790 795 800

D10

Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu
 805 810 815
 Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu
 820 825 830
 Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys
 835 840 845
 His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly
 850 855 860
 Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr
 865 870 875 880
 Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu
 885 890 895
 Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr
 900 905 910
 His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr
 915 920 925
 Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu
 930 935 940
 Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly
 945 950 955 960
 Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val
 965 970 975
 Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu
 980 985 990
 Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu
 995 1000 1005
 Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln
 1010 1015 1020
 Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu
 1025 1030 1035 1040
 Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His
 1045 1050 1055
 Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp
 1060 1065 1070
 Thr Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser
 1075 1080 1085
 Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln
 1090 1095 1100
 Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val

1105 1110 1115 1120

Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu
 1125 1130 1135

Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala
 1140 1145 1150

Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1155 1160 1165

<210> 67
 <211> 3173
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Truncated Protein (ver.2); with Introns Y, Alpha,
 Beta and 2

<400> 67

atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
 gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
 cgcggggacc cggcggtttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
 gacgcacggc cggccccccg cgccccctcc ttccgccagg tgggcctccc cggggtcggc 240
 gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgaggagag cagcgaggc 300
 gactcagggc gcttcccccg caggtgtcct gcctgaagga gctggtggcc cgagtgtgc 360
 agaggtctgt cgagcgcggc gcgaagaacg tgctggcctt cggcttcgcg ctgctggacg 420
 gggcccgcg gggccccccc gaggccttca ccaccagcg gcgcagctac ctgcccaca 480
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<210> 68

<211> 982

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 3 (ver.2); encoded by SEQ ID
NO:67 with Intron Y ORF1

<400> 68

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His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
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Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
65 70 75 80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
85 90 95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
130 135 140

Pro Pro Glu Ala Phe Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
195 200 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
210 215 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
225 230 235 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
245 250 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
260 265 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
275 280 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
290 295 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
305 310 315 320

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
340 345 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
355 360 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
370 375 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
385 390 395 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
405 410 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
420 425 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
450 455 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg

D10

465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
 740 745 750
 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
 755 760 765
 Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
 770 775 780

D10

Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu
 785 790 795 800
 Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu
 805 810 815
 Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu
 820 825 830
 Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys
 835 840 845
 His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly
 850 855 860
 Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr
 865 870 875 880
 Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu
 885 890 895
 Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr
 900 905 910
 His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr
 915 920 925
 Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu
 930 935 940
 Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly
 945 950 955 960
 Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val
 965 970 975
 Gln Ser Asp Tyr Ser Arg
 980

<210> 69
 <211> 897
 <212> PRT
 <213> Homo sapiens

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 NO:67 with Intron Y ORF2 after the termination
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Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
 35 40 45
 Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
 50 55 60
 Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
 65 70 75 80
 Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
 85 90 95
 Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
 100 105 110
 Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
 115 120 125
 Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
 130 135 140
 Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
 145 150 155 160
 Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
 165 170 175
 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
 180 185 190
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
 195 200 205
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
 210 215 220
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
 225 230 235 240
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
 245 250 255
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
 260 265 270
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
 275 280 285
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
 290 295 300
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
 305 310 315 320
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
 325 330 335
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys

Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp
 660 665 670
 Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr
 675 680 685
 Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val
 690 695 700
 Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro
 705 710 715 720
 Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg
 725 730 735
 Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser
 740 745 750
 Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg
 755 760 765
 Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser
 770 775 780
 Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn
 785 790 795 800
 Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val
 805 810 815
 Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe
 820 825 830
 Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn
 835 840 845
 Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly
 850 855 860
 Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys
 865 870 875 880
 Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser
 885 890 895

Arg

<210> 70
 <211> 982
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein 3 (Ver.2); encoded by SEQ ID
 NO:67 with Intron Y ORF3

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His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
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Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
65 70 75 80

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
85 90 95

Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
195 200 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
210 215 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
225 230 235 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
245 250 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
260 265 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
275 280 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
290 295 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
305 310 315 320

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
340 345 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
355 360 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
370 375 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
385 390 395 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
405 410 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
420 425 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
450 455 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
465 470 475 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
485 490 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
500 505 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
530 535 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
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 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
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 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
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 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
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 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
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 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
 755 760 765
 Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
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 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu
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 Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu
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 Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu
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 Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys
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 His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly
 850 855 860
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 Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu
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 Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr
 900 905 910
 His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr

915

920

925

Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu
 930 935 940

Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly
 945 950 955 960

Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val
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Gln Ser Asp Tyr Ser Arg
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<210> 71

<211> 3466

<212> DNA

<213> Homo sapiens

<220>

<223> Altered C-Terminus Protein (ver.2); with Introns
 Y, Alpha, Beta and 3

<400> 71

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 ccctgggtccg aggtgtccct gagtatggct gcgtgggtgaa cttgcggaag acagtgggtga 2820
 acttccctgt agaagacgag gccctgggtg gcacggcttt tgttcagatg ccggccccacg 2880
 gcctattccc ctggtgcggc ctgctgctgg ataccggac cctggagggtg cagagcgact 2940
 actccagcta tgcccggacc tccatcagag ccagtctcac cttcaaccgc ggcttcaagg 3000
 ctggggaggaa catgcgtcgc aaactctttg gggctctgcg gctgaagtgt cacagcctgt 3060
 ttctggattt gcaggtgaac agcctccaga cgggtgtgcac caacatctac aagatcctcc 3120
 tgctgcaggc gtacaggttt cagcatgtg tgctgcagct cccatttcat cagcaagttt 3180
 ggaagaaccc cacatttttc ctgcgctca tctctgacac ggcctccctc tgctactcca 3240
 tcctgaaagc caagaacgca gccgaagaaa acatttctgt cgtgactcct gcggtgcttg 3300
 ggctcgggaca gccagagatg gagccacccc gcagaccgtc ggggtgtgggc agctttccgg 3360
 tgtctcctgg gaggggagtt gggctgggccc tgtgactcct cagcctctgt tttccccccag 3420
 ggatgtcgct gggggccaag ggcgccgccc gccctctgcc ctccga 3466

<210> 72

<211> 1130

<212> PRT

<213> Homo sapiens

<220>

<223> Altered C-Terminus Protein (ver.2); encoded by SEQ
ID NO:71 with Intron Y ORF1

<400> 72

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
65 70 75 80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
85 90 95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys

115 120 125
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165 170 175
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430

D10

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735

Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
 740 745 750
 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
 755 760 765
 Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
 770 775 780
 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu
 785 790 795 800
 Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu
 805 810 815
 Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu
 820 825 830
 Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys
 835 840 845
 His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly
 850 855 860
 Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr
 865 870 875 880
 Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu
 885 890 895
 Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr
 900 905 910
 His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr
 915 920 925
 Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu
 930 935 940
 Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly
 945 950 955 960
 Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val
 965 970 975
 Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu
 980 985 990
 Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu
 995 1000 1005
 Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln
 1010 1015 1020
 Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu
 1025 1030 1035 1040
 Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His

1045	1050	1055
Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp		
1060	1065	1070
Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu		
1075	1080	1085
Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro		
1090	1095	1100
Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val		
1105	1110	1115
		1120
Ser Pro Gly Arg Gly Val Gly Leu Gly Leu		
1125	1130	

<210> 73
 <211> 1045
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Altered C-Terminus Protein (ver.2); encoded by SEQ
 ID NO:71 with Intron Y ORF2 after the termination
 codon

<400> 73

Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr		
1	5	10
		15
Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg		
20	25	30
Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe		
35	40	45
Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe		
50	55	60
Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu		
65	70	75
		80
Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp		
85	90	95
Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala		
100	105	110
Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly		
115	120	125
Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg		
130	135	140
Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly		
145	150	155
		160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
 165 170 175
 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
 180 185 190
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
 195 200 205
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
 210 215 220
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
 225 230 235 240
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
 245 250 255
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
 260 265 270
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
 275 280 285
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
 290 295 300
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
 305 310 315 320
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
 325 330 335
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
 340 345 350
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
 355 360 365
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
 370 375 380
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
 385 390 395 400
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
 405 410 415
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
 420 425 430
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
 435 440 445
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
 450 455 460

D10

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
465 470 475 480

Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
485 490 495

Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
500 505 510

Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
515 520 525

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
530 535 540

Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
545 550 555 560

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
565 570 575

Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
580 585 590

Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
595 600 605

Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
610 615 620

Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
625 630 635 640

Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr
645 650 655

Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp
660 665 670

Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr
675 680 685

Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val
690 695 700

Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro
705 710 715 720

Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg
725 730 735

Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser
740 745 750

Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg
755 760 765

Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser

D10

770 775 780
 Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn
 785 790 795 800
 Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val
 805 810 815
 Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe
 820 825 830
 Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn
 835 840 845
 Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly
 850 855 860
 Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys
 865 870 875 880
 Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser
 885 890 895
 Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly
 900 905 910
 Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg
 915 920 925
 Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln
 930 935 940
 Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr Arg
 945 950 955 960
 Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys
 965 970 975
 Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys
 980 985 990
 Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu Glu Asn Ile Leu Val
 995 1000 1005
 Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro Glu Met Glu Pro Pro
 1010 1015 1020
 Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val Ser Pro Gly Arg Gly
 1025 1030 1035 1040
 Val Gly Leu Gly Leu
 1045

<210> 74
 <211> 1130
 <212> PRT
 <213> Homo sapiens

<220>

<223> Altered C-Terminus Protein (ver.2); encoded by SEQ
ID NO:71 with Intron Y ORF3

<400> 74

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
65 70 75 80

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
85 90 95

Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
195 200 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
210 215 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
225 230 235 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
245 250 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
260 265 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly

D10

275	280	285
Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe 290	295	300
Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu 305	310	315
Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln 325	330	335
His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp 340	345	350
Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser 355	360	365
Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu 370	375	380
Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu 385	390	395
Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu 405	410	415
Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly 420	425	430
Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro 435	440	445
Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys 450	455	460
Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg 465	470	475
Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr 485	490	495
Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp 500	505	510
Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe 515	520	525
Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp 530	535	540
Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val 545	550	555
Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala 565	570	575
Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg 580	585	590

D10

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
 740 745 750
 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
 755 760 765
 Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
 770 775 780
 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu
 785 790 795 800
 Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu
 805 810 815
 Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu
 820 825 830
 Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys
 835 840 845
 His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly
 850 855 860
 Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr
 865 870 875 880
 Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu
 885 890 895

Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr
900 905 910

His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr
915 920 925

Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu
930 935 940

Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly
945 950 955 960

Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val
965 970 975

Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu
980 985 990

Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu
995 1000 1005

Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln
1010 1015 1020

Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu
1025 1030 1035 1040

Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His
1045 1050 1055

Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp
1060 1065 1070

Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu
1075 1080 1085

Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro
1090 1095 1100

Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val
1105 1110 1115 1120

Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
1125 1130

<210> 75

<211> 4022

<212> DNA

<213> Homo sapiens

<220>

<223> Protein Lacking Motif A (ver.2); with Introns Y
and Beta

<400> 75

atgccgcgcg cccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctgggtgcag 120

cgcggggacc cggcggtttt cgcgcgcgtg gtggcccagt gcctgggtgtg cgtgccctgg 180
 gacgcacggc cgccccccgc cgcacctcc ttccgccagg tgggctccc cggggtcggc 240
 gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
 gactcagggc gcttcccccg caggtgtcct gcctgaagga gctgggtggc cgagtgtctg 360
 agaggtgtg cgagcgcggc gcgaagaacg tgctggcctt cggcttcgcg ctgctggacg 420
 gggcccgcg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaaca 480
 cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtgggcg 540
 acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctgggt gctcccagct 600
 gcgcctacca ggtgtgcggg ccgcgcgtgt accagctcgg cgtgccact caggccccggc 660
 ccccgccaca cgctagtggg cccgaaggc gtctgggatg cgaacggggc tggaaaccata 720
 gcgtcagggg ggcgggggtc cccctgggccc tgccagcccc ggggtgcgagg aggcgcgggg 780
 gcagtgccag ccgaagtctg ccgttgccca agaggccag gcgtggcgct gcccctgagc 840
 cggagcggac gcccgttggg caggggtcct gggccacccc gggcaggacg cgtgggacga 900
 gtgaccgtgg tttctgtgtg gtgtcacctg ccagaccgc cgaagaagcc acctctttgg 960
 aggggtgcgt ctctggcacg cgcactccc accatccgt gggccgccag caccacgcgg 1020
 gccccccatc cacatcgcg ccaccacgtc cctgggacac gccttgtccc cgggtgtacg 1080
 ccgagaccaa gcacttctc tactctcag gcgacaagga gcagctgcgg cctccttcc 1140
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 tgggttccag gccctggatg ccagggactc cccgcaggtt gccccgctg cccagcgct 1260
 actggcaaat cgggccccctg tttctggagc tgcttgggaa ccacgcgcag tgccccctacg 1320
 ggggtgctcct caagacgcac tgcccgtgc gagctgcggt caccacagca gccggtgtct 1380
 gtgcccggga gaagccccag ggctctgtgg cggccccga ggaggaggac acagaccccc 1440
 gtgcctgggt gcagctgctc cgccagcaca gcagcccctg gcaggtgtac ggcttcgtgc 1500
 gggcctgcct gcgcggctg gtgccccag gcctctgggg ctccaggcac aacgaacgcc 1560
 gcttccctcag gaacaccaag aagttcatct ccctggggaa gcatgccaag ctctcgtgc 1620
 aggagctgac gtggaagatg agcgtgcggg actgcgctt gctgcgcagg agcccagggg 1680
 ttggctgtgt tccggccgca gagcaccgtc tgctgagga gatcctggcc aagttcctgc 1740
 actggctgat gagtgtgtac gtcgtcgagc tgctcaggtc tttcttttat gtcacggaga 1800
 ccacgtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaa 1860
 gcattggaat cagacagcac ttgaagaggg tgagctgcg ggagctgtcg gaagcagagg 1920
 tcaggcagca tcgggaagcc aggccgccc tgctacgtc cagactccgc ttcacccca 1980
 agcctgacgg gctgcggccg attgtgaaca tggactcgt cgtgggagcc agaacttcc 2040
 gcagagaaaa gagggccgag cgtctcacct cgagggtgaa ggactgttc agcgtgctca 2100
 actacgagcg ggcgcggcgc cccggcctcc tgggcgcctc tgtgctgggc ctggacgata 2160
 tccacagggc ctggcgacac ttctgtgtgc gtgtgcgggc ccaggacccg ccgctgagc 2220
 tgtactttgt caaggacagg ctacgaggg tcatcgccag catcatcaa cccagaaca 2280
 cgtactgcgt gcgtcggtat gccgtggtcc agaaggccgc ccattgggac gtccgcaagg 2340
 ccttcaagag ccacgtctct accttgacag acctccagcc gtacatgca cagttcgtgg 2400
 ctcacctgca ggagaccagc ccgctgaggg atgccgtcgt catcgagcag agctcctccc 2460
 tgaatgagge cagcagtggc ctcttcgacg tcttctacg cttcatgtgc caccacgccg 2520
 tgccatcag gggcaagtc tactccagt gccaggggat cccgcagggc tccatcctct 2580
 ccacgtgct ctgcagcctg tgctacggcg acatggagaa caagctgttt gcggggattc 2640
 ggcgggacgg gctgctcctg cgtttgggtg atgatttctt gttggtgaca cctcacctca 2700
 cccacgcgaa aaccttctc aggacctgg tccgaggtgt ccctgagtat ggctgcgtgg 2760
 tgaacttgcg gaagacagt gtgaacttcc ctgtagaaga cgaggccctg ggtggcacgg 2820
 cttttgttca gatgccggcc cacggcctat tcccctgggt cggcctgctg ctggataccc 2880
 ggaccttga ggtgcagagc gactactcca gctatgccc gacctccatc agagccagtc 2940
 tcaccttcaa ccgcggttcc aaggtggga ggaacatgcg tcgcaaacctc tttggggtct 3000
 tgcggtgaa gtgtcacagc ctgtttctgg atttgcaggt gaacagcctc cagacggtgt 3060
 gcaccaacat ctacaagatc ctctgtgc aggegtacag gtttcacgca tgtgtgctgc 3120
 agtcccatt tcactagcaa gtttgaaga accccatt tttcctgcgc gtcactctctg 3180
 acacggcctc cctctgtac tccatcctga aagccaagaa cgcagggatg tcgctggggg 3240
 ccaagggcgc cgccggccct ctgcccctcg aggcgtgca gtggctgtgc caccaagcat 3300
 tcctgtcaa gctgactcga caccgtgtca cctacgtgcc actcctgggg tcaactcagga 3360
 cagcccagac gcagctgagt cggaagctcc cggggacgac gctgactgcc ctggaggccg 3420
 cagccaaccc ggcactgccc tcagacttca agaccatcct ggactgatgg ccaccgcgcc 3480
 acagccaggc cgagagcaga caccagcagc cctgtcacgc cgggctctac gtcccaggga 3540
 gggaggggcg gcccacaccc aggcccgcac cgtgggagt ctgaggcctg agtgagtgtt 3600

D10

tggccgaggc ctgcatgtcc ggctgaaggc tgagtgtccg gctgaggcct gagcgagtgt 3660
 ccagccaagg gctgagtgtc cagcacacct gccgtcttca cttccccaca ggctggcgct 3720
 cggctccacc ccagggccag ctttttctca ccaggagccc ggcttccact cccacatag 3780
 gaatagtcca tccccagatt cgccattgtt caccctctgc cctgccctcc tttgccttcc 3840
 acccccacca tccaggtgga gaccctgaga aggaccctgg gagctctggg aatttgaggt 3900
 gaccaaaggt gtgccctgta cacaggcgag gaccctgcac ctggatgggg gtccctgtgg 3960
 gtcaaattgg ggggaggtgc tgtgggagta aaatactgaa tatatgagtt tttcagtttt 4020
 ga 4022

<210> 76

<211> 1154

<212> PRT

<213> Homo sapiens

<220>

<223> Protein Lacking Motif A (ver.2); encoded by SEQ ID
 NO:75 with Intron Y ORF1

<400> 76

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
 65 70 75 80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
 85 90 95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
 100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205

D10

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe

515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala
 740 745 750
 Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
 755 760 765
 Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His
 770 775 780
 Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
 785 790 795 800
 His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln
 805 810 815
 Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu
 820 825 830

D10

Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val
 835 840 845
 Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys
 850 855 860
 Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg
 865 870 875 880
 Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr
 885 890 895
 Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly
 900 905 910
 Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn
 915 920 925
 Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met
 930 935 940
 Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg
 945 950 955 960
 Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile
 965 970 975
 Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met
 980 985 990
 Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe
 995 1000 1005
 Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr
 1010 1015 1020
 Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln
 1025 1030 1035 1040
 Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg
 1045 1050 1055
 Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys
 1060 1065 1070
 Asn Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro
 1075 1080 1085
 Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu
 1090 1095 1100
 Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr
 1105 1110 1115 1120
 Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala
 1125 1130 1135

Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile
 1140 1145 1150

Leu Asp

<210> 77
 <211> 1069
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Protein Lacking Motif A (ver.2); encoded by SEQ ID
 NO:75 with Intron Y ORF2 after the termination
 codon

<400> 77
 Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
 1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
 20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
 35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
 50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
 100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
 115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
 130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
 145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
 165 170 175

Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
 180 185 190

Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
 195 200 205

Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro

Did

210 215 220
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
 225 230 235 240
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
 245 250 255
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
 260 265 270
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
 275 280 285
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
 290 295 300
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
 305 310 315 320
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
 325 330 335
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
 340 345 350
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
 355 360 365
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
 370 375 380
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
 385 390 395 400
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
 405 410 415
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
 420 425 430
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
 435 440 445
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
 450 455 460
 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
 465 470 475 480
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
 485 490 495
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
 500 505 510
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
 515 520 525

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
 530 535 540
 Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
 545 550 555 560
 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
 565 570 575
 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
 580 585 590
 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
 595 600 605
 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
 610 615 620
 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
 625 630 635 640
 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr
 645 650 655
 Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro
 660 665 670
 Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala
 675 680 685
 His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr
 690 695 700
 Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr
 705 710 715 720
 Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn
 725 730 735
 Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His
 740 745 750
 His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile
 755 760 765
 Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly
 770 775 780
 Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu
 785 790 795 800
 Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His
 805 810 815
 Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly
 820 825 830

Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp
 835 840 845
 Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu
 850 855 860
 Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln
 865 870 875 880
 Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr
 885 890 895
 Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe
 900 905 910
 Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val
 915 920 925
 Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu
 930 935 940
 Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln
 945 950 955 960
 Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr
 965 970 975
 Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser
 980 985 990
 Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln
 995 1000 1005
 Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val
 1010 1015 1020
 Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu
 1025 1030 1035 1040
 Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala
 1045 1050 1055
 Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1060 1065

<210> 78

<211> 1154

<212> PRT

<213> Homo sapiens

<220>

<223> Protein Lacking Motif A (ver.2); encoded by SEQ ID
NO:75 with Intron Y ORF3

<400> 78

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
 65 70 75 80
 Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
 85 90 95
 Gln Arg Arg Arg Leu Arg Ala Leu Pro Gln Val Ser Cys Leu Lys
 100 105 110
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165 170 175
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val

625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala
 740 745 750
 Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
 755 760 765
 Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His
 770 775 780
 Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
 785 790 795 800
 His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln
 805 810 815
 Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu
 820 825 830
 Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val
 835 840 845
 Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys
 850 855 860
 Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg
 865 870 875 880
 Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr
 885 890 895
 Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly
 900 905 910
 Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn
 915 920 925
 Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met
 930 935 940

D10

Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg
 945 950 955 960
 Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile
 965 970 975
 Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met
 980 985 990
 Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe
 995 1000 1005
 Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr
 1010 1015 1020
 Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln
 1025 1030 1035 1040
 Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg
 1045 1050 1055
 Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys
 1060 1065 1070
 Asn Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro
 1075 1080 1085
 Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu
 1090 1095 1100
 Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr
 1105 1110 1115 1120
 Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala
 1125 1130 1135
 Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile
 1140 1145 1150
 Leu Asp

<210> 79

<211> 3137

<212> DNA

<213> Homo sapiens

<220>

<223> Truncated Protein Lacking Motif A (ver.2); with
 Introns Y, Beta and 2

<400> 79

atgccgcgcgc ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
 gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
 cgcggggacc cggcggttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
 gacgcacggc cgccccccgc cgccccctcc ttccgccagg tgggcctccc cggggtcggc 240

gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
gactcagggc gcttcccccg caggtgtcct gcctgaagga gctggtggcc cgagtgtgc 360
agaggtgtg cgagcgcggc gcgaagaacg tgctggcctt cggcttcgcg ctgctggacg 420
gggcccgcgg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaca 480
cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtgggcg 540
acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600
gcgcctacca ggtgtgcggg ccgcgcgtgt accagctcgg cgctgccact caggcccggc 660
ccccgccaca cgctagtga ccccggaagg gtctgggatg cgaacggggc tggaaaccata 720
gcgtcagggg ggcgggggtc cccctggggc tgccagcccc ggggtgcgagg aggcgcgggg 780
gcagtgccag ccgaagtctg ccgttgcccc agaggcccc gctggtgcgt gccctgagc 840
cggagcggac gcccgttggg caggggtcct gggccccccc gggcaggacg cgtggaccga 900
gtgaccgtgg tttctgtgtg gtgtcacctg ccagaccgcg cgaagaagcc acctctttg 960
aggggtgcgt ctctggcacg cgcactccc acccatccgt gggccgcccag caccagcag 1020
gccccccatc cacatcgcg ccaccacgtc cctgggacac gccttgtccc ccggtgtcg 1080
ccgagaccaa gcaattcctc tactcctcag gcgacaagga gcagctgcgg cctccttcc 1140
tactcagctc tctgaggccc agcctgactg gcgctcggag gctcgtggag accatcttcc 1200
tgggttccag gccctggatg ccagggactc cccgcagggt gcccgcctg cccagcgt 1260
actggcaaat gcggcccctg tttctggagc tgcttgggaa ccacgcgcag tgcccctacg 1320
gggtgctcct caagacgcac tgcccgtgc gagctgcggt caccacagca gccggtgtct 1380
gtgcccggga gaagccccag ggctctgtgg cggcccccca ggaggaggac acagaccccc 1440
gtgcctgggt gcagctgctc gcagccccag gcagccccgt gcaggtgtac ggcttcgtgc 1500
gggctgctc gcgcgggctg gtgccccag cctctgtggg ctccaggcac aacgaacgcc 1560
gcttctcag gaacaccaag aagttcatct cctggggaa gcatgccaaag ctctcgtgc 1620
aggagctgac gtggaagatg agcgtgcggg actgcgctt gctgcgcagg agcccagggg 1680
ttggctgtgt tccggccgca gagcacctg tgctgagga gatcctggcc aagttcctgc 1740
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ccacgtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaaa 1860
gcattggaat cagacagcac ttgaagaggg tgcagctgcg ggagctgtcg gaagcagagg 1920
tcaggcagca tcgggaagcc aggcgcgccc tgctgacgtc cagactccgc ttcaccccca 1980
agcctgacgg gctgcggccg attgtgaaca tggactacgt cgtgggagcc agaacgttcc 2040
gcagagaaaa gagggccgag cgtctcacct cgagggtgaa ggcactgttc agcgtgctca 2100
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tccacagggc ctggcgacac ttctgtgtgc gtgtgcgggc ccaggaccgc ccgcctgagc 2220
tgtactttgt caaggacagg ctacaggagg tcatcgccag catcatcaaa cccagaaca 2280
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tgaacttgcg gaagacagt gtgaacttcc ctgtagaaga cgaggccctg ggtggacagg 2820
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ggcaggcgac tgccaatccc aaagggtcag atgccacagg gtgcccctcg tcccatctgg 3060
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<210> 80

<211> 970

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein lacking Motif A (ver.2); encoded
by SEQ ID NO:79 with Intron Y ORF1

<400> 80

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1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
65 70 75 80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
85 90 95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
195 200 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
210 215 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
225 230 235 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
245 250 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
260 265 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
275 280 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
290 295 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605

D10

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala
 740 745 750
 Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
 755 760 765
 Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His
 770 775 780
 Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
 785 790 795 800
 His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln
 805 810 815
 Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu
 820 825 830
 Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val
 835 840 845
 Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys
 850 855 860
 Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg
 865 870 875 880
 Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr
 885 890 895
 Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly
 900 905 910
 Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn

915

920

925

Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met
 930 935 940

Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg
 945 950 955 960

Thr Leu Glu Val Gln Ser Asp Tyr Ser Arg
 965 970

<210> 81

<211> 885

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein lacking Motif A (ver.2); encoded
 by SEQ ID NO:79 with Intron Y ORF2 after the
 termination codon

<400> 81

Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
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Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
 20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
 35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
 50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
 100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
 115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
 130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
 145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
 165 170 175

Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
 180 185 190

Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
 195 200 205
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
 210 215 220
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
 225 230 235 240
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
 245 250 255
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
 260 265 270
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
 275 280 285
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
 290 295 300
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
 305 310 315 320
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
 325 330 335
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
 340 345 350
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
 355 360 365
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
 370 375 380
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
 385 390 395 400
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
 405 410 415
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
 420 425 430
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
 435 440 445
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
 450 455 460
 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
 465 470 475 480
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
 485 490 495

Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
500 505 510

Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
515 520 525

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
530 535 540

Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
545 550 555 560

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
565 570 575

Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
580 585 590

Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
595 600 605

Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
610 615 620

Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
625 630 635 640

Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr
645 650 655

Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro
660 665 670

Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala
675 680 685

His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr
690 695 700

Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr
705 710 715 720

Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn
725 730 735

Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His
740 745 750

His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile
755 760 765

Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly
770 775 780

Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu
785 790 795 800

Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His

805 810 815
 Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly
 820 825 830
 Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp
 835 840 845
 Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu
 850 855 860
 Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln
 865 870 875 880
 Ser Asp Tyr Ser Arg
 885

<210> 82
 <211> 970
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein lacking Motif A (ver.2); encoded
 by SEQ ID NO:79 with Intron Y ORF3

<400> 82
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
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 His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
 65 70 75 80
 Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
 85 90 95
 Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
 100 105 110
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165 170 175
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg

465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala
 740 745 750
 Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
 755 760 765
 Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His
 770 775 780

D10

Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
 785 790 795 800
 His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln
 805 810 815
 Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu
 820 825 830
 Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val
 835 840 845
 Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys
 850 855 860
 Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg
 865 870 875 880
 Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr
 885 890 895
 Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly
 900 905 910
 Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn
 915 920 925
 Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met
 930 935 940
 Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg
 945 950 955 960
 Thr Leu Glu Val Gln Ser Asp Tyr Ser Arg
 965 970

<210> 83

<211> 3432

<212> DNA

<213> Homo sapiens

<220>

<223> Protein Lacking Motif A and Altered C-Terminus
 (ver.2); with Intron Y, Beta and 3

<400> 83

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 ccacgctgct ctgcagcctg tgctacggcg acatggagaa caagctgttt gcggggattc 2640
 gggcgggacgg gctgctcctg cgtttggtgg atgatttctt gttggtgaca cctcacctca 2700
 cccacgcgaa aaccttctc aggacctggg tccgaggtgt ccctgagtat ggctgcgtgg 2760
 tgaacttgcg gaagacagtg gtgaacttcc ctgtagaaga cgaggccctg ggtggcacgg 2820
 cttttgttca gatgccggcc caccggcctat tcccctggtg cggcctgctg ctggataccc 2880
 ggaccttga ggtgcagagc gactactcca gctatgcccg gacctccatc agagccagtc 2940
 tcaccttcaa ccgcggctc aaggctggga ggaacatgcg tcgcaaactc tttggggtct 3000
 tgccgctgaa gtgtcacagc ctggttcttg atttgcaggg gaacagcctc cagacgggtg 3060
 gcaccaacat ctacaagatc ctctgctgc aggcgtacag gtttcacgca tgtgtgctgc 3120
 agctcccatt tcatcagcaa gtttggaga accccacatt tttcctgcgc gtcattctctg 3180
 acacggcctc cctctgctac tccatcctga aagccaagaa cgcagccgaa gaaaacattt 3240
 ctgtcgtgac tctgcggtg cttgggtcgg gacagccaga gatggagcca cccgcagac 3300
 cgtcgggtgt gggcagcttt ccggtgtctc ctgggagggg agttgggctg ggctgtgac 3360
 tctcagcct ctgttttccc ccagggatgt cgctgggggc caagggcgcc gccggccctc 3420
 tgccctccga ga 3432

<210> 84

<211> 1122

<212> PRT

<213> Homo sapiens

<220>

<223> Protein Lacking Motif A and Altered C-Terminus
 (ver.2); encoded by SEQ ID NO:83 with Intron Y
 ORF1

<400> 84

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15
His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30
Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45
Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
65 70 75 80
Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
85 90 95
Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
100 105 110
Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125
Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
130 135 140
Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145 150 155 160
Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
165 170 175
Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
180 185 190
Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
195 200 205
Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
210 215 220
Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
225 230 235 240
Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
245 250 255
Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
260 265 270
Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
275 280 285
Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
290 295 300

D10

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
305 310 315 320

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
340 345 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
355 360 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
370 375 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
385 390 395 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
405 410 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
420 425 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
450 455 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
465 470 475 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
485 490 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
500 505 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
530 535 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala
 740 745 750
 Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
 755 760 765
 Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His
 770 775 780
 Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
 785 790 795 800
 His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln
 805 810 815
 Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu
 820 825 830
 Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val
 835 840 845
 Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys
 850 855 860
 Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg
 865 870 875 880
 Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr
 885 890 895
 Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly
 900 905 910
 Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn

915 920 925
 Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met
 930 935 940
 Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg
 945 950 955 960
 Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile
 965 970 975
 Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met
 980 985 990
 Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe
 995 1000 1005
 Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr
 1010 1015 1020
 Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln
 1025 1030 1035 1040
 Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg
 1045 1050 1055
 Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys
 1060 1065 1070
 Asn Ala Glu Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly
 1075 1080 1085
 Ser Gly Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly
 1090 1095 1100
 Ser Phe Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu Phe Ile
 1105 1110 1115 1120
 Gly Ala

<210> 85
 <211> 1037
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Protein Lacking Motif A and Altered C-Terminus
 (ver.2); encoded by SEQ ID NO:83 with Intron Y
 ORF2 after the termination codon

<400> 85
 Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
 1 5 10 15
 Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
 20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
 35 40 45
 Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
 50 55 60
 Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
 65 70 75 80
 Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
 85 90 95
 Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
 100 105 110
 Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
 115 120 125
 Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
 130 135 140
 Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
 145 150 155 160
 Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
 165 170 175
 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
 180 185 190
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
 195 200 205
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
 210 215 220
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
 225 230 235 240
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
 245 250 255
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
 260 265 270
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
 275 280 285
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
 290 295 300
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
 305 310 315 320
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
 325 330 335

D18

Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
 340 345 350
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
 355 360 365
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
 370 375 380
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
 385 390 395 400
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
 405 410 415
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
 420 425 430
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
 435 440 445
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
 450 455 460
 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
 465 470 475 480
 D10 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
 485 490 495
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
 500 505 510
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
 515 520 525
 Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
 530 535 540
 Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
 545 550 555 560
 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
 565 570 575
 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
 580 585 590
 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
 595 600 605
 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
 610 615 620
 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
 625 630 635 640
 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr

645										650										655													
Phe	Val	Lys	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile	Lys	Pro																		
			660						665						670																		
Gln	Asn	Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala	Ala																		
			675						680						685																		
His	Gly	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser	Thr	Leu	Thr																		
			690						695						700																		
Asp	Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu	Gln	Glu	Thr																		
			705						710						720																		
Ser	Pro	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser	Ser	Leu	Asn																		
									725						730																		
Glu	Ala	Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	Arg	Phe	Met	Cys	His																		
									740						745																		
His	Ala	Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val	Gln	Cys	Gln	Gly	Ile																		
									755						760																		
Pro	Gln	Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu	Cys	Tyr	Gly																		
									770						775																		
Asp	Met	Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp	Gly	Leu	Leu																		
									785						790																		
Leu	Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr	His																		
									805						810																		
Ala	Lys	Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr	Gly																		
									820						825																		
Cys	Val	Val	Asn	Leu	Arg	Lys	Thr	Val	Val	Asn	Phe	Pro	Val	Glu	Asp																		
									835						840																		
Glu	Ala	Leu	Gly	Gly	Thr	Ala	Phe	Val	Gln	Met	Pro	Ala	His	Gly	Leu																		
									850						855																		
Phe	Pro	Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	Thr	Leu	Glu	Val	Gln																		
									865						870																		
Ser	Asp	Tyr	Ser	Ser	Tyr	Ala	Arg	Thr	Ser	Ile	Arg	Ala	Ser	Leu	Thr																		
									885						890																		
Phe	Asn	Arg	Gly	Phe	Lys	Ala	Gly	Arg	Asn	Met	Arg	Arg	Lys	Leu	Phe																		
									900						905																		
Gly	Val	Leu	Arg	Leu	Lys	Cys	His	Ser	Leu	Phe	Leu	Asp	Leu	Gln	Val																		
									915						920																		
Asn	Ser	Leu	Gln	Thr	Val	Cys	Thr	Asn	Ile	Tyr	Lys	Ile	Leu	Leu	Leu																		
									930						935																		
Gln	Ala	Tyr	Arg	Phe	His	Ala	Cys	Val	Leu	Gln	Leu	Pro	Phe	His	Gln																		
									945						950																		
															955																		
															960																		

D10

Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr
965 970 975

Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu Glu
980 985 990

Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro Glu
995 1000 1005

Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val Ser
1010 1015 1020

Pro Gly Arg Gly Val Gly Leu Gly Leu Phe Ile Gly Ala
1025 1030 1035

<210> 86

<211> 1122

<212> PRT

<213> Homo sapiens

<220>

<223> Protein Lacking Motif A and Altered C-Terminus
(ver.2); encoded by SEQ ID NO:83 with Intron Y
ORF3

<400> 86

210 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
65 70 75 80

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
85 90 95

Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165 170 175
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg

465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 D18 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala
 740 745 750
 Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
 755 760 765
 Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His
 770 775 780

Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
785 790 795 800

His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln
805 810 815

Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu
820 825 830

Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val
835 840 845

Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys
850 855 860

Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg
865 870 875 880

Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr
885 890 895

Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly
900 905 910

Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn
915 920 925

D/D

Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met
930 935 940

Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg
945 950 955 960

Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile
965 970 975

Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met
980 985 990

Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe
995 1000 1005

Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr
1010 1015 1020

Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln
1025 1030 1035 1040

Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg
1045 1050 1055

Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys
1060 1065 1070

Asn Ala Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly
1075 1080 1085

Ser Gly Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly
 1090 1095 1100

Ser Phe Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu Phe Ile
 1105 1110 1115 1120

Gly Ala

<210> 87
 <211> 7615
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Human Telomerase Clone with Exon Beta Spliced Out

<400> 87
 tcgacctgca ggcatgcaag cttggcactg gccgtcgttt tacaacgtcg tgactgggaa 60
 aaccctggcg ttacccaact taatcgccct gcagcacatc cccctttcgc cagctggcgt 120
 aatagcgaag agggccgcac cgatcgccct tcccaacagt tgcgcagcct gaatggcgaa 180
 tggcgccctga tgcgggtatct tctccttacg catctgtgcg gtatttcaca ccgcataaat 240
 tccctgtttt ggcgggatgag agaagatttt cagcctgata cagattaaat cagaacgcag 300
 aagcgggtctg ataaaacaga atttgcctgg cggcagtagc gcggtgggtcc cacctgaccc 360
 catgccgaac tcagaagtga aacgccgtag cgccgatggg agtgtggggg ctccccatgc 420
 gagagtaggg aactgccagg catcaaataa aacgaaaggc tcagtcgaaa gactggggcct 480
 ttcgttttat ctggtgtttg tcggtgaacg ctctcctgag taggacaaat ccgccgggag 540
 cggatttgaa cggttgcgaag caacggcccc gaggggtggcg ggcaggacgc ccgccataaa 600
 ctgccaggca tcaaattaag cagaaggcca tcctgacgga tggccttttt gcgtttctac 660
 aaactcttcc tgtcgtcata tctacaagcc atccccccac agatacggta aactgcctc 720
 gtttttgcac caggaaagca gggaatttat ggtgcactct cagtacaatc tgctctgatg 780
 ccgcatagtt aagccagccc cgacaccgcg caacaccgcg tgacgcgccc tgacgggctt 840
 gtctgctccc ggcatccgct tacagacaag ctgtgaccgt ctccgggagc tgcatgtgtc 900
 agagggtttt accgtcatca ccgaaacgcg cgagacgaaa gggcctcgtg atacgcctat 960
 ttttataggt taatgtcatg ataataatgg tttcttagac gtgaggttct gtacccgaca 1020
 ccatcgaatg gtgcaaaacc tttcgcggtg tggcatgata gcgcccggaa gagagtcaat 1080
 tcagggtggg gaatgtgaaa ccagtaacgt tatacagatg cgcagagtat gccggtgtct 1140
 cttatcagac cgtttcccgcc gtggtgaacc aggccagcca cgtttctgcg aaaacgcggg 1200
 aaaaatggga agcggcgatg gcggagctga attacattcc caaccgcgtg gcacaacaac 1260
 tggcggggcaa acagtcgttg ctgattggcg ttgccacctc cagtctggcc ctgcacgcgc 1320
 cgtcgcaaat tgtcgcggcg attaaatctc gcgccgatca actgggtgcc agcgtggtgg 1380
 tgtcgatggg agaacgaagc ggcgtcgaag cctgtaaaag ggcggtgcac aatcttctcg 1440
 cgcaacgcgt cagtgggctg atcattaact atccgctgga tgaccaggat gccattgctg 1500
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<213> Homo sapiens

<220>

<223> Human Telomerase Clone with exon Alpha Spliced Out

<400> 89

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<210> 90
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<213> Homo sapiens

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<400> 90
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D10

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<210> 91
<211> 8
<212> PRT
<213> Unknown

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<223> Description of Unknown Organism: Consensus P-loop
      Motif Sequence found in large number of protein
      families

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<220>
<221> MOD_RES
<222> (2)..(5)
<223> Wherein Xaa is any residue

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<400> 91
Ala Xaa Xaa Xaa Xaa Gly Lys Ser
 1                               5

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<210> 92
<211> 17
<212> PRT
<213> Homo sapiens

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Gly

<210> 93
<211> 9
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown Organism: Consensus c-Alb
SH3 binding peptide

<220>

<221> MOD_RES
<222> (2)..(5)
<223> Wherein Xaa is any residue

<220>

<221> MOD_RES
<222> (7)..(8)
<223> Wherein Xaa is any residue

<400> 93

Pro Xaa Xaa Xaa Xaa Pro Xaa Xaa Pro
1 5

D10
<210> 94
<211> 17
<212> PRT
<213> Homo sapiens

<400> 94

His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr
1 5 10 15

Pro

<210> 95
<211> 14
<212> DNA
<213> Unknown

<220>

<223> Description of Unknown Organism: General Target
Sequence Recognized by Hairpin Ribozyme

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<222> (1)..(3)
<223> Wherein N is G, U, C or A

<220>

<221> modified_base

<222> (5)
<223> Wherein N is G, U, C or A

<220>
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<222> (9)..(14)
<223> Wherein N is G, U, C or A

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14

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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Amplification
Primer Design Based on EST Sequence GenBank
Accession Number AA281296

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26

<210> 97
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Amplification
Primer Design Based on EST Sequence GenBank
Accession Number AA281296

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21

<210> 98
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Amplification
Primer Design Based on EST Sequence GenBank
Accession Number AA281296

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20

<210> 99
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Amplification
Primer Design Based on EST Sequence GenBank

Accession Number AA281296

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<210> 100
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

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<210> 101
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<212> DNA
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Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

D/O
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GenBank Accession Number AA281296

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<212> DNA
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GenBank Accession Number AA281296

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GenBank Accession Number AA281296

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GenBank Accession Number AA281296

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Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

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GenBank Accession Number AA281296

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GenBank Accession Number AA281296

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<210> 116
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GenBank Accession Number AA281296

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<210> 117
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 117
gtacatgcga cagttcgtgg ctca

24

<210> 118
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 118
catgaagcgt aggaagacgt cgaaga

26

<210> 119
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 119
cgcaaacage ttgttctcca tgtc

24

<210> 120
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 120
ctatgcccgg acctccatca ga

22

<210> 121
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 121
ctgatggagg tccgggcata g

21

D10

<210> 122
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 122
cctccgaggc cgtgcagt 18

<210> 123
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 123
cacctcaagc tttctagatc agtccaggat ggtccttgaag tca 43

<210> 124
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 124
ggaaggcaaa ggagggcagg gcga 24

<210> 125
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 125
cacgaattcg gatccaagct tttttttttt tttttttt 37

<210> 126
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 126

gggttgcgga gggtgggc

18

<210> 127

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 127

gcagtgggtga gccgagtcct g

21

<210> 128

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 128

cgactttgga ggtgccttca

20

<210> 129

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 129

gctgggtgcag cgcgggggacc

20

<210> 130

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 130

gaggtgcaga gcgactactc ca

22

<210> 131

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 131

gtctcacctc gaggggtgaag

20

<210> 132

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 132

ggctgctcct gcgtttggtg ga

22

<210> 133

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 133

gccagagatg gagccaccc

19

<210> 134

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 134

gggtggctcc atctctggc

19

<210> 135

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 135

ccgcacgctc atcttccacg t

21

<210> 136

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 136

gcttggggat gaagcggtc

19

<210> 137

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 137

cgccctgagct gtactttgtc a

21

<210> 138

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 138

cacctcaagc tttctagatc agctagcggc ccagcccaac tcccct

46

<210> 139

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 139
gcagcacaca tgcgtgaaac ctgt 24

<210> 140
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 140
gtgtcagaga tgacgcgcag gaa 23

<210> 141
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

D18 <400> 141
accacactt gcctgtcctg agt 23

<210> 142
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 142
actggatcct tgacaattaa tgcacgcggt cgtataatgt gtggagggtt gcggagggtg 60
ggc 63

<210> 143
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 143
ctgtaatacg actcactata gggttcgga gggtgggc 38

<210> 144
<211> 73

<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 144
cacctgcaga catgcgtttc gtcctcacgg actcatcagg ccagctggcg acgcatgtgt 60
gagccgagtc ctg 73

<210> 145
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 145
ggatccgccg cagagcaccg tctg 24

D10
<210> 146
<211> 29
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 146
cgaagctttc agtggggccgg catctgaac 29

<210> 147
<211> 29
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 147
cgaagctttc acaggcccag cccaactcc 29

<210> 148
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized

Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 148
gcggatccag agccacgtcc tacgtc 26

<210> 149
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 149
gcggatccgt tcagatgccg gcccac 26

<210> 150
<211> 9
<212> PRT
<213> Homo sapiens

<400> 150
Pro Glu Met Glu Pro Pro Arg Arg Pro
1 5

<210> 151
<211> 4
<212> PRT
<213> Homo sapiens

<400> 151
Ala Ala Glu His
1

<210> 152
<211> 6
<212> PRT
<213> Homo sapiens

<400> 152
Val Gln Met Pro Ala His
1 5

<210> 153
<211> 5
<212> PRT
<213> Homo sapiens

<400> 153
Val Gly Leu Gly Leu
1 5

<210> 154
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 154
 Arg Ala Thr Ser
 1

<210> 155
 <211> 622
 <212> PRT
 <213> Homo sapiens

<220>
 <223> N-Terminal Truncated Telomerase (ver.2); encoded
 by SEQ ID NO:51, with Y Intron ORF3

<400> 155
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15
 His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
 65 70 75 80
 Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
 85 90 95
 Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
 100 105 110
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165 170 175
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro

195 200 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
210 215 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
225 230 235 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
290 295 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
305 310 315 320

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
370 375 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
385 390 395 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
450 455 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
465 470 475 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510

D10

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
530 535 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
545 550 555 560

DP Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly
610 615 620
